

ENTERED



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RAW SEQUENCE LISTING

DATE: 08/15/2003

PATENT APPLICATION: US/09/922,185

TIME: 14:40:01

Input Set : N:\Crf3\RULE60\09922185.raw.txt

Output Set: N:\CRF4\08152003\I922185.raw

SEQUENCE LISTING

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1 (1) GENERAL INFORMATION:
2   (i) APPLICANT: Robertson, Dan E.
3           Sanyal, Indrajit
4           Adhikari, Robert S.
5   (ii) TITLE OF INVENTION: CATALASES
6   (iii) NUMBER OF SEQUENCES: 8
7   (iv) CORRESPONDENCE ADDRESS:
8           (A) ADDRESSEE: Fish & Richardson P.C.
9           (B) STREET: 4225 Executive Square, Suite 1400
10          (C) CITY: La Jolla
11          (D) STATE: CA
12          (E) COUNTRY: US
13          (F) ZIP: 92037
14   (v) COMPUTER READABLE FORM:
15          (A) MEDIUM TYPE: Diskette
16          (B) COMPUTER: IBM Compatible
17          (C) OPERATING SYSTEM: Windows95
18          (D) SOFTWARE: FastSEQ for Windows Version 2.0
19   (vi) CURRENT APPLICATION DATA:
C--> 20          (A) APPLICATION NUMBER: US/09/922,185
C--> 21          (B) FILING DATE: 02-Aug-2001
22   (vii) PRIOR APPLICATION DATA:
W--> 23          (A) APPLICATION NUMBER: 09/412,347
24          (B) FILING DATE: 25-OCT-1999
W--> 25          (A) APPLICATION NUMBER: 08/674,887
26          (B) FILING DATE:
27   (viii) ATTORNEY/AGENT INFORMATION:
28          (A) NAME: Haile, Ph.D., Lisa A.
29          (B) REGISTRATION NUMBER: 38,347
30          (C) REFERENCE/DOCKET NUMBER: 09015/002001
31   (ix) TELECOMMUNICATION INFORMATION:
32          (A) TELEPHONE: 619/678-5070
33          (B) TELEFAX: 619/678-5099
34 (2) INFORMATION FOR SEQ ID NO: 1:
35   (i) SEQUENCE CHARACTERISTICS:
36          (A) LENGTH: 52 base pairs
37          (B) TYPE: nucleic acid
38          (C) STRANDEDNESS: single
39          (D) TOPOLOGY: linear
W--> 40   (ii) MOLECULE TYPE: pcr primer
41   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
42       CCGAGAATTC ATTAAGAGG AGAAATTAAC TATGAATAAC GCATCCGCTG AC

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44 (2) INFORMATION FOR SEQ ID NO: 2:
45     (i) SEQUENCE CHARACTERISTICS:
46         (A) LENGTH: 31 base pairs
47         (B) TYPE: nucleic acid
48         (C) STRANDEDNESS: single
49         (D) TOPOLOGY: linear
W--> 50     (ii) MOLECULE TYPE: pcr primer
51     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
52         CGGAAAGCTT TTACGACGCG ACGTCGAAAC G                               31
54 (2) INFORMATION FOR SEQ ID NO: 3:
55     (i) SEQUENCE CHARACTERISTICS:
56         (A) LENGTH: 52 base pairs
57         (B) TYPE: nucleic acid
58         (C) STRANDEDNESS: single
59         (D) TOPOLOGY: linear
W--> 60     (ii) MOLECULE TYPE: pcr primer
61     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
62         CCGAGAATTC ATTAAGAGG AGAAATTAAC TATGGAAAAT CACAAACACT CA       52
64 (2) INFORMATION FOR SEQ ID NO: 4:
65     (i) SEQUENCE CHARACTERISTICS:
66         (A) LENGTH: 31 base pairs
67         (B) TYPE: nucleic acid
68         (C) STRANDEDNESS: single
69         (D) TOPOLOGY: linear
W--> 70     (ii) MOLECULE TYPE: pcr primer
71     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
72         CGAAGGTACC TTATTCAGA TCAAACCGGT C                               31
74 (2) INFORMATION FOR SEQ ID NO: 5:
75     (i) SEQUENCE CHARACTERISTICS:
76         (A) LENGTH: 2262 base pairs
77         (B) TYPE: nucleic acid
78         (C) STRANDEDNESS: double
79         (D) TOPOLOGY: linear
80     (ii) MOLECULE TYPE: cDNA
81     (ix) FEATURE:
82         (A) NAME/KEY: Coding Sequence
83         (B) LOCATION: 1...2259
84     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
85         ATG AAT AAC GCA TCC GCT GAC GAT CTA CAC AGT AGC TTG CAG CAA AGA       48
86         Met Asn Asn Ala Ser Ala Asp Asp Leu His Ser Ser Leu Gln Gln Arg
87         1           5           10           15
88         TGC AGA GCA TTT GTT CCC TTG GTA TCG CCA AGG CAT AGA GCA ATA AGG       96
89         Cys Arg Ala Phe Val Pro Leu Val Ser Pro Arg His Arg Ala Ile Arg
90         20           25           30
91         GAG AGA GCT ATG AGC GGT AAA TGT CCT GTC ATG CAC GGT GGT AAC ACC       144
92         Glu Arg Ala Met Ser Gly Lys Cys Pro Val Met His Gly Gly Asn Thr
93         35           40           45
94         TCG ACC GGT ACT TCC AAC AAA GAT TGG TGG CCG GAA GGG TTG AAC CTG       192
95         Ser Thr Gly Thr Ser Asn Lys Asp Trp Trp Pro Glu Gly Leu Asn Leu

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Input Set : N:\Crf3\RULE60\09922185.raw.txt

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96	50	55	60	
97	GAT ATT TTG CAT CAG CAA GAT CGC AAA TCA GAC CCG ATG GAT CCG GAT	240		
98	Asp Ile Leu His Gln Gln Asp Arg Lys Ser Asp Pro Met Asp Pro Asp			
99	65 70 75 80			
100	TTC AAC TAC CGT GAA GAA GTA CGC AAG CTC GAT TTC GAC GCG CTG AAG	288		
101	Phe Asn Tyr Arg Glu Glu Val Arg Lys Leu Asp Phe Asp Ala Leu Lys			
102	85 90 95			
103	AAA GAT GTC CAC GCG TTG ATG ACC GAT AGC CAA GAG TGG TGG CCC GCT	336		
104	Lys Asp Val His Ala Leu Met Thr Asp Ser Gln Glu Trp Trp Pro Ala			
105	100 105 110			
106	GAC TGG GGG CAC TAC GGC GGT TTG ATG ATC CGT ATG GCT TGG CAC TCC	384		
107	Asp Trp Gly His Tyr Gly Gly Leu Met Ile Arg Met Ala Trp His Ser			
108	115 120 125			
109	GCT GGC ACC TAC CGT ATT GCT GAT GGC CGT GGG GGC GGT GGT ACC GGA	432		
110	Ala Gly Thr Tyr Arg Ile Ala Asp Gly Arg Gly Gly Gly Thr Gly			
111	130 135 140			
112	AGC CAG CGC TTT GCA CCG CTC AAC TCC TGG CCG GAC AAC GTC AGC CTG	480		
113	Ser Gln Arg Phe Ala Pro Leu Asn Ser Trp Pro Asp Asn Val Ser Leu			
114	145 150 155 160			
115	GAT AAA GCG CGC CGT CTG CTG TGG CCG ATC AAG AAG AAG TAC GGC AAC	528		
116	Asp Lys Ala Arg Arg Leu Leu Trp Pro Ile Lys Lys Lys Tyr Gly Asn			
117	165 170 175			
118	AAA ATC AGC TGG GCA GAC CTG ATG ATT CTG GCT GGC ACC GTG GCT TAT	576		
119	Lys Ile Ser Trp Ala Asp Leu Met Ile Leu Ala Gly Thr Val Ala Tyr			
120	180 185 190			
121	GAG TCC ATG GGC TTA CCT GCT TAC GGC TTC TCT TTC GGC CGC GTC GAT	624		
122	Glu Ser Met Gly Leu Pro Ala Tyr Gly Phe Ser Phe Gly Arg Val Asp			
123	195 200 205			
124	ATT TGG GAA CCC GAA AAA GAT ATC TAC TGG GGT GAC GAA AAA GAG TGG	672		
125	Ile Trp Glu Pro Glu Lys Asp Ile Tyr Trp Gly Asp Glu Lys Glu Trp			
126	210 215 220			
127	CTG GCA CCT TCT GAC GAA CGC TAC GGC GAC GTG AAC AAG CCA GAG ACC	720		
128	Leu Ala Pro Ser Asp Glu Arg Tyr Gly Asp Val Asn Lys Pro Glu Thr			
129	225 230 235 240			
130	ATG GAA AAC CCG CTG GCG GCT GTC CAA ATG GGT CTG ATC TAT GTG AAC	768		
131	Met Glu Asn Pro Leu Ala Ala Val Gln Met Gly Leu Ile Tyr Val Asn			
132	245 250 255			
133	CCG GAA GGT GTT AAC GGC CAC CCT GAT CCG CTG AGA ACC GCA CAG CAG	816		
134	Pro Glu Gly Val Asn Gly His Pro Asp Pro Leu Arg Thr Ala Gln Gln			
135	260 265 270			
136	GTA CTT GAA ACC TTC GCC CGT ATG GCG ATG AAC GAC GAA AAA ACC GCA	864		
137	Val Leu Glu Thr Phe Ala Arg Met Ala Met Asn Asp Glu Lys Thr Ala			
138	275 280 285			
139	GCC CTC ACA GCT GGC GGC CAC ACC GTC GGT AAT TGT CAC GGT AAT GGC	912		
140	Ala Leu Thr Ala Gly Gly His Thr Val Gly Asn Cys His Gly Asn Gly			
141	290 295 300			
142	AAT GCC TCT GCG TTA GCC CCT GAC CCA AAA GCC TCT GAC GTT GAA AAC	960		
143	Asn Ala Ser Ala Leu Ala Pro Asp Pro Lys Ala Ser Asp Val Glu Asn			
144	305 310 315 320			

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145	CAG GGC TTA GGT TGG GGC AAC CCC AAC ATG CAG GGC AAG GCA AGC AAC	1008
146	Gln Gly Leu Gly Trp Gly Asn Pro Asn Met Gln Gly Lys Ala Ser Asn	
147	325 330 335	
148	GCC GTG ACC TCG GGT ATC GAA GGT GCT TGG ACC ACC AAC CCC ACG AAA	1056
149	Ala Val Thr Ser Gly Ile Glu Gly Ala Trp Thr Thr Asn Pro Thr Lys	
150	340 345 350	
151	TTC GAT ATG GGC TAT TTC GAC CTG CTG TTC GGC TAC AAT TGG GAA CTG	1104
152	Phe Asp Met Gly Tyr Phe Asp Leu Leu Phe Gly Tyr Asn Trp Glu Leu	
153	355 360 365	
154	AAA AAG AGT CCT GCC GGT GCC CAC CAT TGG GAA CCG ATT GAC ATC AAA	1152
155	Lys Lys Ser Pro Ala Gly Ala His His Trp Glu Pro Ile Asp Ile Lys	
156	370 375 380	
157	AAG GAA AAC AAG CCG GTT GAC GCC AGC GAC CCC TCT ATT CGC CAC AAC	1200
158	Lys Glu Asn Lys Pro Val Asp Ala Ser Asp Pro Ser Ile Arg His Asn	
159	385 390 395 400	
160	CCG ATC ATG ACC GAT GCG GAT ATG GCG ATA AAG GTA AAT CCG ACC TAT	1248
161	Pro Ile Met Thr Asp Ala Asp Met Ala Ile Lys Val Asn Pro Thr Tyr	
162	405 410 415	
163	CGC GCT ATC TGC GAA AAA TTC ATG GCC GAT CCT GAG TAC TTC AAG AAA	1296
164	Arg Ala Ile Cys Glu Lys Phe Met Ala Asp Pro Glu Tyr Phe Lys Lys	
165	420 425 430	
166	ACT TTC GCG AAG GCG TGG TTC AAG CTG ACG CAC CGT GAC CTG GGC CCG	1344
167	Thr Phe Ala Lys Ala Trp Phe Lys Leu Thr His Arg Asp Leu Gly Pro	
168	435 440 445	
169	AAA TCA CGT TAC ATC GGC CCG GAA GTG CCG GCA GAA GAC CTG ATT TGG	1392
170	Lys Ser Arg Tyr Ile Gly Pro Glu Val Pro Ala Glu Asp Leu Ile Trp	
171	450 455 460	
172	CAA GAC CCG ATT CCG GCA GGT AAC ACC GAC TAC TGC GAA GAA GTG GTC	1440
173	Gln Asp Pro Ile Pro Ala Gly Asn Thr Asp Tyr Cys Glu Glu Val Val	
174	465 470 475 480	
175	AAG CAG AAA ATT GCA CAA AGT GGC CTG AGC ATT AGT GAG ATG GTC TCC	1488
176	Lys Gln Lys Ile Ala Gln Ser Gly Leu Ser Ile Ser Glu Met Val Ser	
177	485 490 495	
178	ACC GCT TGG GAC AGT GCC CGT ACT TAT CGC GGT TCC GAT ATG CGC GGC	1536
179	Thr Ala Trp Asp Ser Ala Arg Thr Tyr Arg Gly Ser Asp Met Arg Gly	
180	500 505 510	
181	GGT GCT AAC GGT GCC CGC ATT CGC TTG GCC CCA CAG AAC GAG TGG CAG	1584
182	Gly Ala Asn Gly Ala Arg Ile Arg Leu Ala Pro Gln Asn Glu Trp Gln	
183	515 520 525	
184	GGC AAC GAG CCG GAG CGC CTG GCG AAA GTG CTG AGC GTC TAC GAG CAG	1632
185	Gly Asn Glu Pro Glu Arg Leu Ala Lys Val Leu Ser Val Tyr Glu Gln	
186	530 535 540	
187	ATC TCT GCC GAC ACC GGC GCT AGC ATC GCG GAC GTG ATC GTT CTG GCC	1680
188	Ile Ser Ala Asp Thr Gly Ala Ser Ile Ala Asp Val Ile Val Leu Ala	
189	545 550 555 560	
190	GGT AGC GTA GGC ATC GAG AAA GCC GCG AAA GCA GCA GGT TAC GAT GTG	1728
191	Gly Ser Val Gly Ile Glu Lys Ala Ala Lys Ala Ala Gly Tyr Asp Val	
192	565 570 575	
193	CGC GTT CCC TTC CTG AAA GGC CGT GGC GAT GCG ACC GCC GAG ATG ACC	1776

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194 Arg Val Pro Phe Leu Lys Gly Arg Gly Asp Ala Thr Ala Glu Met Thr
195          580          585          590
196 GAC GCA GAC TCC TTC GCA CCG CTG GAG CCG CTG GCC GAT GGC TTC CGC 1824
197 Asp Ala Asp Ser Phe Ala Pro Leu Glu Pro Leu Ala Asp Gly Phe Arg
198          595          600          605
199 AAC TGG CAG AAG AAA GAG TAT GTG GTG AAG CCG GAA GAG ATG CTG CTG 1872
200 Asn Trp Gln Lys Lys Glu Tyr Val Val Lys Pro Glu Glu Met Leu Leu
201          610          615          620
202 GAT CGT GCG CAG CTG ATG GGC TTA ACC GGC CCG GAA ATG ACC GTG CTG 1920
203 Asp Arg Ala Gln Leu Met Gly Leu Thr Gly Pro Glu Met Thr Val Leu
204          625          630          635          640
205 CTG GGC GGT ATG CGC GTA CTG GGC ACC AAC TAT GGT GGC ACC AAA CAC 1968
206 Leu Gly Gly Met Arg Val Leu Gly Thr Asn Tyr Gly Gly Thr Lys His
207          645          650          655
208 GGC GTA TTC ACC GAT TGT GAA GGC CAG TTG ACC AAC GAC TTT TTT GTG 2016
209 Gly Val Phe Thr Asp Cys Glu Gly Gln Leu Thr Asn Asp Phe Phe Val
210          660          665          670
211 AAC CTG ACC GAT ATG GGG AAC AGC TGG AAG CCG GTA GGT AGC AAC GCC 2064
212 Asn Leu Thr Asp Met Gly Asn Ser Trp Lys Pro Val Gly Ser Asn Ala
213          675          680          685
214 TAC GAA ATC CGC GAC CGC AAG ACC GGT GCC GTG AAG TGG ACC GCC TCG 2112
215 Tyr Glu Ile Arg Asp Arg Lys Thr Gly Ala Val Lys Trp Thr Ala Ser
216          690          695          700
217 CGG GTG GAT CTG GTA TTT GGT TCC AAC TCG CTA CTG CGC TCT TAC GCA 2160
218 Arg Val Asp Leu Val Phe Gly Ser Asn Ser Leu Leu Arg Ser Tyr Ala
219          705          710          715          720
220 GAA GTG TAC GCC CAG GAC GAT AAC GGC GAG AAG TTC GTC AGA GAC TTC 2208
221 Glu Val Tyr Ala Gln Asp Asp Asn Gly Glu Lys Phe Val Arg Asp Phe
222          725          730          735
223 GTC GCC GCC TGG ACC AAA GTG ATG AAC GCC GAC CGT TTC GAC GTC GCG 2256
224 Val Ala Ala Trp Thr Lys Val Met Asn Ala Asp Arg Phe Asp Val Ala
225          740          745          750
226 TCG TAA 2262
227 Ser
229 (2) INFORMATION FOR SEQ ID NO: 6:
230 (i) SEQUENCE CHARACTERISTICS:
231 (A) LENGTH: 753 amino acids
232 (B) TYPE: amino acid
233 (D) TOPOLOGY: linear
234 (ii) MOLECULE TYPE: protein
235 (v) FRAGMENT TYPE: internal
236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
237 Met Asn Asn Ala Ser Ala Asp Asp Leu His Ser Ser Leu Gln Gln Arg
238 1 5 10 15
239 Cys Arg Ala Phe Val Pro Leu Val Ser Pro Arg His Arg Ala Ile Arg
240 20 25 30
241 Glu Arg Ala Met Ser Gly Lys Cys Pro Val Met His Gly Gly Asn Thr
242 35 40 45
243 Ser Thr Gly Thr Ser Asn Lys Asp Trp Trp Pro Glu Gly Leu Asn Leu

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VERIFICATION SUMMARY

DATE: 08/15/2003

PATENT APPLICATION: US/09/922,185

TIME: 14:40:02

Input Set : N:\CrF3\RULE60\09922185.raw.txt

Output Set: N:\CRF4\08152003\I922185.raw

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:25 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)
L:40 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:50 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:60 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:70 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4

STATISTICS SUMMARY

PATENT APPLICATION: US/09/922,185

DATE: 08/15/2003

TIME: 14:40:02

Input Set : N:\CrF3\RULE60\09922185.raw.txt

Output Set: N:\CRF4\08152003\I922185.raw

Application Serial Number: US/09/922,185

Alpha or Numeric or Xml: Alpha

Application Class:

Application File Date: 08-02-2001

Art Unit: OIPE

Software Application: FastSEQ2.0

Total Number of Sequences: 8

Total Nucleotides: 4666

Total Amino Acids: 1498

Number of Errors: 0

Number of Warnings: 5

Number of Corrections: 2

MESSAGE SUMMARY

220 C: 2 (Keyword misspelled or invalid format)

246 W: 4 (Invalid value of Alpha Sequence Header Field)